

No new matter is added by these amendments.

In the Claims

Please cancel claims 10, 15, 20-25, 27, and 31 without prejudice to further prosecution.

Please amend the claims as follows:

*P2*  
*A3*  
*Sub 3*

1. (Amended) An isolated nucleic acid fragment comprising a sequence of at least about 10 nucleotides from a Brassicaceae or Helianthus delta-12 fatty acid desaturase gene having at least one mutation in a region of said desaturase gene encoding a His-Xaa-Xaa-His amino acid motif, wherein said [gene is effective for altering fatty acid composition in Brassicaceae or Helianthus seeds] at least one mutation renders the product of said desaturase gene non-functional and wherein said sequence includes said at least one mutation.

3. (Amended) The nucleic acid fragment of claim 2, wherein said at least one mutation [comprises] in said gene introduces a non-conservative amino acid substitution in said [region] motif.

*A4*  
*Sub 4*

4. (Amended) An isolated nucleic acid fragment comprising a sequence of at least about 10 nucleotides from a Brassicaceae or Helianthus delta-15 fatty acid desaturase gene having at least one mutation in a region of said desaturase gene encoding a His-Xaa-Xaa-His amino acid motif, wherein said [gene is effective for altering fatty acid composition in Brassicaceae or Helianthus seeds] at least one mutation renders the product of said desaturase gene non-functional and wherein said sequence includes said at least one mutation.

6. (Amended) The nucleic acid fragment of claim 5, wherein said at least one mutation [comprises] in said gene introduces a non-conservative amino acid substitution in said [region] motif.

*A4*

7. (Amended) An isolated nucleic acid fragment encoding a polypeptide having an amino acid sequence selected from the group consisting of: [an amino acid sequence substantially identical to] SEQ ID NO:12, [an amino acid sequence substantially identical to] and SEQ ID NO:16 [and an amino acid sequence substantially identical to SEQ ID NO:18].

11. (Amended) An isolated nucleic acid fragment, wherein said nucleic acid  
fragment is selected from the group consisting of:

- A5
- a) SEQ ID NO:11;
  - b) SEQ ID NO:15;
  - c)[ SEQ ID NO:17;
  - d)] an RNA [analog] comprising a nucleotide sequence of SEQ ID NO:11,  
wherein uracil replaces thymine;
  - [e]d) an RNA [analog] comprising a nucleotide sequence of SEQ ID NO:15,  
wherein uracil replaces thymine;
  - [f] an RNA analog of SEQ ID NO:17;
  - g)e) a nucleic acid fragment having a nucleic acid sequence complementary to a),  
b), c), or d)[, e), or f)]; and
  - [h]f) a nucleic acid fragment of a), b), c), d), or e)[, f), or g),] that is at least 10  
nucleotides in length and that hybridizes under stringent conditions to genomic DNA encoding  
the mutation in the polypeptide of SEQ ID NO:12, or SEQ ID NO:16[, or SEQ ID NO:18].

12. (Amended) An isolated polypeptide having an amino acid sequence selected  
from the group consisting of: [an amino acid sequence substantially identical to] SEQ ID  
NO:12[,] and [an amino acid sequence substantially identical to] SEQ ID NO:16[, and an amino  
acid sequence substantially identical to SEQ ID NO:18].

A6

16. (Amended) A Brassicaceae or Helianthus plant, said plant containing first and  
second delta-12 fatty acid desaturase genes, each said gene having at least one mutation, wherein  
at least one of said mutations is in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif  
and wherein each said mutation renders the product of said desaturase gene non-functional, and  
confers an altered fatty acid composition in seeds of said plant.

In claim 18, please delete "region" and insert therefor --motif--.

26. (Amended) A method for producing a Brassicaceae or Helianthus plant line, comprising the steps of:

- a) inducing mutagenesis in cells of a starting variety of a Brassicaceae or Helianthus species;
  - b) obtaining one or more progeny plants from said cells;
  - c) identifying at least one of said progeny plants that contain[s] a delta-12 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif, and wherein said mutation renders the product of said desaturase gene non-functional; and
  - d) producing said plant line from said at least one progeny plant by self- or cross-pollination, said plant line having said at least one delta-12 gene mutation and producing seeds yielding an oil having a linoleic acid content from about 1% to about 14%.

28. (Amended) The method of claim 26, further comprising the steps of:

- e) inducing mutagenesis in cells of said plant line;
  - f) obtaining one or more progeny plants from said plant line cells;
  - g) identifying at least one of said plant line progeny plants that contains a delta-15 fatty acid desaturase gene having at least one delta-15 gene mutation, said at least one delta-15 gene mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif, wherein said mutation renders the product of said delta-15 desaturase gene non-functional;
  - h) producing a second plant line from said at least one plant line progeny plant by self- or cross-pollination, said second plant line having said at least one delta-12 gene mutation and said at least one delta-15 gene mutation and producing seeds yielding an oil having a linoleic acid content from about 1% to about 14%.

30. (Amended) A method for producing a Brassicaceae plant line, comprising the steps of:

- a) inducing mutagenesis in cells of a starting variety of a Brassicaceae species;
  - b) obtaining one or more progeny plants from said cells;

*AP  
Conc'd*

c) identifying at least one of said progeny plants that contains a delta-12 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif, wherein said at least one mutation renders the product of said desaturase gene non-functional;

d) producing a first plant line from said at least one progeny plant by self- or cross-pollination, said plant line having said at least one delta-12 gene mutation;

e) inducing mutagenesis in cells of said first plant line;

f) obtaining one or more progeny plants from said first plant line cells;

g) identifying at least one of said first plant line progeny plants that contains a second delta-12 fatty acid desaturase gene having at least one mutation, said second gene mutation in a region other than a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif; and

h) producing a second plant line from said at least one plant line progeny plant by self- or cross-pollination, said second plant line having said first delta-12 gene mutation and said second delta-12 gene mutation.

*A10 F*

Please add the following new claims.

35. The nucleic acid fragment of claim 11, wherein said nucleic acid fragment is SEQ ID NO: 11.

36. The nucleic acid fragment of claim 11, wherein said nucleic acid fragment is SEQ ID NO: 15.

37. The plant of claim 16, wherein said plant is a Brassicaceae plant.

38. The plant of claim 37, wherein said plant is a Brassica napus plant.

*Sub 39*

39. The plant of claim 37, wherein said motif comprises the sequence His-Glu-Cys-Gly-His.

40. The plant of claim 37, wherein said mutation comprises a non-conservative amino acid substitution in said motif.

41. The method of claim 26, wherein said starting variety is a Brassicaceae species.

*Sub 40*

42. The method of claim 41, wherein said identifying step comprises identifying a mutation in a His-Glu-Cys-Gly-His amino acid motif.

43. The method of claim 28, wherein said starting variety is a Brassicaceae species variety.